

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Borowsky, Beth
- (ii) TITLE OF INVENTION: DNA ENCODING A HUMAN Ob RECEPTOR (hOb-Re) AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Cooper & Dunham LLP
  - (B) STREET: 1185 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: USA
  - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: White, John P
  - (B) REGISTRATION NUMBER: 28,678
  - (C) REFERENCE/DOCKET NUMBER: 1795-53801/JPW/KDB
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 212 278 0400
  - (B) TELEFAX: 212 291 0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..54
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAT GTT AAA AAG TTT CAC ATC CAC GGT ATG TGT ACT GTA CTT TTC ATG 48  
Asn Val Lys Lys Phe His Ile His Gly Met Cys Thr Val Leu Phe Met  
1 5 10 15

GAT TAG

54

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Asp \*

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asn	Val	Lys	Lys	Phe	His	Ile	His	Gly	Met	Cys	Thr	Val	Leu	Phe	Met
1				5					10					15	

Asp \*

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCT	GTT	AAG	AAG	TAT	TAT	ATC	CAT	GGT	AAG	TTT	ACT	ATA	CTT	TAG	
Ser	Val	Lys	Lys	Tyr	Tyr	Ile	His	Gly	Lys	Phe	Thr	Ile	Leu	*	45
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser	Val	Lys	Lys	Tyr	Tyr	Ile	His	Gly	Lys	Phe	Thr	Ile	Leu	*
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGT ATG TGT ACT GTA CTT TTC ATG GAT  
Gly Met Cys Thr Val Leu Phe Met Asp  
1 5

27

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Met Cys Thr Val Leu Phe Met Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGT AAG TTT ACT ATA CTT  
Gly Lys Phe Thr Ile Leu  
10 15

18

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Lys Phe Thr Ile Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG	ATT	TGT	CAA	AAA	TTC	TGT	GTG	GTT	TTG	TTA	CAT	TGG	GAA	TTT	ATT	48
Met	Ile	Cys	Gln	Lys	Phe	Cys	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Ile	
1				5					10					15		
TAT	GTG	ATA	ACT	GCG	TTT	AAC	TTG	TCA	TAT	CCA	ATT	ACT	CCT	TGG	AGA	96
Tyr	Val	Ile	Thr	Ala	Phe	Asn	Leu	Ser	Tyr	Pro	Ile	Thr	Pro	Trp	Arg	
			20				25						30			
TTT	AAG	TTG	TCT	TGC	ATG	CCA	CCA	AAT	TCA	ACC	TAT	GAC	TAC	TTC	CTT	144
Phe	Lys	Leu	Ser	Cys	Met	Pro	Pro	Asn	Ser	Thr	Tyr	Asp	Tyr	Phe	Leu	
		35					40					45				
TTG	CCT	GCT	GGA	CTC	TCA	AAG	AAT	ACT	TCA	AAT	TCG	AAT	GGA	CAT	TAT	192
Leu	Pro	Ala	Gly	Leu	Ser	Lys	Asn	Thr	Ser	Asn	Ser	Asn	Gly	His	Tyr	
	50					55					60					
GAG	ACA	GCT	GTT	GAA	CCT	AAG	TTT	AAT	TCA	AGT	GGT	ACT	CAC	TTT	TCT	240
Glu	Thr	Ala	Val	Glu	Pro	Lys	Phe	Asn	Ser	Ser	Gly	Thr	His	Phe	Ser	
	65				70				75						80	
AAC	TTA	TCC	AAA	ACA	ACT	TTC	CAC	TGT	TGC	TTT	CGG	AGT	GAG	CAA	GAT	288
Asn	Leu	Ser	Lys	Thr	Thr	Phe	His	Cys	Cys	Phe	Arg	Ser	Glu	Gln	Asp	
			85					90						95		
AGA	AAC	TGC	TCC	TTA	TGT	GCA	GAC	AAC	ATT	GAA	GGA	AAG	ACA	TTT	GTT	336
Arg	Asn	Cys	Ser	Leu	Cys	Ala	Asp	Asn	Ile	Glu	Gly	Lys	Thr	Phe	Val	
			100					105					110			
TCA	ACA	GTA	AAT	TCT	TTA	GTT	TTT	CAA	CAA	ATA	GAT	GCA	AAC	TGG	AAC	384
Ser	Thr	Val	Asn	Ser	Leu	Val	Phe	Gln	Gln	Ile	Asp	Ala	Asn	Trp	Asn	
			115				120					125				
ATA	CAG	TGC	TGG	CTA	AAA	GGA	GAC	TTA	AAA	TTA	TTC	ATC	TGT	TAT	GTG	432
Ile	Gln	Cys	Trp	Leu	Lys	Gly	Asp	Leu	Lys	Leu	Phe	Ile	Cys	Tyr	Val	
	130					135					140					
GAG	TCA	TTA	TTT	AAG	AAT	CTA	TTC	AGG	AAT	TAT	AAC	TAT	AAG	GTC	CAT	480

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Glu 145	Ser	Leu	Phe	Lys	Asn 150	Leu	Phe	Arg	Asn	Tyr 155	Asn	Tyr	Lys	Val	His 160	
CTT	TTA	TAT	GTT	CTG	CCT	GAA	GTG	TTA	GAA	GAT	TCA	CCT	CTG	GTT	CCC	528
Leu	Leu	Tyr	Val	Leu 165	Pro	Glu	Val	Leu	Glu 170	Asp	Ser	Pro	Leu 175	Val	Pro	
CAA	AAA	GGC	AGT	TTT	CAG	ATG	GTT	CAC	TGC	AAT	TGC	AGT	GTT	CAT	GAA	576
Gln	Lys	Gly	Ser 180	Phe	Gln	Met	Val	His 185	Cys	Asn	Cys	Ser	Val 190	His	Glu	
TGT	TGT	GAA	TGT	CTT	GTG	CCT	GTG	CCA	ACA	GCC	AAA	CTC	AAC	GAC	ACT	624
Cys	Cys	Glu 195	Cys	Leu	Val	Pro	Val 200	Pro	Thr	Ala	Lys	Leu 205	Asn	Asp	Thr	
CTC	CTT	ATG	TGT	TTG	AAA	ATC	ACA	TCT	GGT	GGA	GTA	ATT	TTC	CAG	TCA	672
Leu	Leu 210	Met	Cys	Leu	Lys	Ile 215	Thr	Ser	Gly	Gly	Val 220	Ile	Phe	Gln	Ser	
CCT	CTA	ATG	TCA	GTT	CAG	CCC	ATA	AAT	ATG	GTG	AAG	CCT	GAT	CCA	CCA	720
Pro	Leu	Met	Ser	Val	Gln 230	Pro	Ile	Asn	Met	Val 235	Lys	Pro	Asp	Pro	Pro 240	
TTA	GGT	TTG	CAT	ATG	GAA	ATC	ACA	GAT	GAT	GGT	AAT	TTA	AAG	ATT	TCT	768
Leu	Gly	Leu	His	Met 245	Glu	Ile	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile 255	Ser	
TGG	TCC	AGC	CCA	CCA	TTG	GTA	CCA	TTT	CCA	CTT	CAA	TAT	CAA	GTG	AAA	816
Trp	Ser	Ser	Pro 260	Pro	Leu	Val	Pro	Phe 265	Pro	Leu	Gln	Tyr	Gln 270	Val	Lys	
TAT	TCA	GAG	AAT	TCT	ACA	ACA	GTT	ATC	AGA	GAA	GCT	GAC	AAG	ATT	GTC	864
Tyr	Ser	Glu 275	Asn	Ser	Thr	Thr	Val 280	Ile	Arg	Glu	Ala	Asp 285	Lys	Ile	Val	
TCA	GCT	ACA	TCC	CTG	CTA	GTA	GAC	AGT	ATA	CTT	CCT	GGG	TCT	TCG	TAT	912
Ser	Ala 290	Thr	Ser	Leu	Leu	Val 295	Asp	Ser	Ile	Leu	Pro 300	Gly	Ser	Ser	Tyr	
GAG	GTT	CAG	GTG	AGG	GGC	AAG	AGA	CTG	GAT	GGC	CCA	GGA	ATC	TGG	AGT	960
Glu	Val	Gln	Val	Arg	Gly 310	Lys	Arg	Leu	Asp	Gly 315	Pro	Gly	Ile	Trp	Ser 320	
GAC	TGG	AGT	ACT	CCT	CGT	GTC	TTT	ACC	ACA	CAA	GAT	GTC	ATA	TAC	TTT	1008
Asp	Trp	Ser	Thr 325	Pro	Arg	Val	Phe	Thr	Thr 330	Gln	Asp	Val	Ile 335	Tyr	Phe	
CCA	CCT	AAA	ATT	CTG	ACA	AGT	GTT	GGG	TCT	AAT	GTT	TCT	TTT	CAC	TGC	1056
Pro	Pro	Lys 340	Ile	Leu	Thr	Ser	Val	Gly 345	Ser	Asn	Val	Ser	Phe 350	His	Cys	
ATC	TAT	AAG	AAG	GAA	AAC	AAG	ATT	GTT	CCC	TCA	AAA	GAG	ATT	GTT	TGG	1104
Ile	Tyr	Lys 355	Lys	Glu	Asn	Lys	Ile 360	Val	Pro	Ser	Lys	Glu 365	Ile	Val	Trp	
TGG	ATG	AAT	TTA	GCT	GAG	AAA	ATT	CCT	CAA	AGC	CAG	TAT	GAT	GTT	GTG	1152
Trp	Met 370	Asn	Leu	Ala	Glu	Lys 375	Ile	Pro	Gln	Ser	Gln 380	Tyr	Asp	Val	Val	
AGT	GAT	CAT	GTT	AGC	AAA	GTT	ACT	TTT	TTC	AAT	CTG	AAT	GAA	ACC	AAA	1200
Ser	Asp	His	Val	Ser	Lys 390	Val	Thr	Phe	Phe	Asn 395	Leu	Asn	Glu	Thr	Lys 400	

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CCT	CGA	GGA	AAG	TTT	ACC	TAT	GAT	GCA	GTG	TAC	TGC	TGC	AAT	GAA	CAT	1248
Pro	Arg	Gly	Lys	Phe	Thr	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	His	
				405					410					415		
GAA	TGC	CAT	CAT	CGC	TAT	GCT	GAA	TTA	TAT	GTG	ATT	GAT	GTC	AAT	ATC	1296
Glu	Cys	His	His	Arg	Tyr	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	
			420					425					430			
AAT	ATC	TCA	TGT	GAA	ACT	GAT	GGG	TAC	TTA	ACT	AAA	ATG	ACT	TGC	AGA	1344
Asn	Ile	Ser	Cys	Glu	Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	
		435					440					445				
TGG	TCA	ACC	AGT	ACA	ATC	CAG	TCA	CTT	GCG	GAA	AGC	ACT	TTG	CAA	TTG	1392
Trp	Ser	Thr	Ser	Thr	Ile	Gln	Ser	Leu	Ala	Glu	Ser	Thr	Leu	Gln	Leu	
	450					455					460					
AGG	TAT	CAT	AGG	AGC	AGC	CTT	TAC	TGT	TCT	GAT	ATT	CCA	TCT	ATT	CAT	1440
Arg	Tyr	His	Arg	Ser	Ser	Leu	Tyr	Cys	Ser	Asp	Ile	Pro	Ser	Ile	His	
465					470					475					480	
CCC	ATA	TCT	GAG	CCC	AAA	GAT	TGC	TAT	TTG	CAG	AGT	GAT	GGT	TTT	TAT	1488
Pro	Ile	Ser	Glu	Pro	Lys	Asp	Cys	Tyr	Leu	Gln	Ser	Asp	Gly	Phe	Tyr	
				485					490					495		
GAA	TGC	ATT	TTC	CAG	CCA	ATC	TTC	CTA	TTA	TCT	GGC	TAC	ACA	ATG	TGG	1536
Glu	Cys	Ile	Phe	Gln	Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	
			500					505					510			
ATT	AGG	ATC	AAT	CAC	TCT	CTA	GGT	TCA	CTT	GAC	TCT	CCA	CCA	ACA	TGT	1584
Ile	Arg	Ile	Asn	His	Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	
	515						520					525				
GTC	CTT	CCT	GAT	TCT	GTG	GTG	AAG	CCA	CTG	CCT	CCA	TCC	AGT	GTG	AAA	1632
Val	Leu	Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Ser	Val	Lys	
	530					535					540					
GCA	GAA	ATT	ACT	ATA	AAC	ATT	GGA	TTA	TTG	AAA	ATA	TCT	TGG	GAA	AAG	1680
Ala	Glu	Ile	Thr	Ile	Asn	Ile	Gly	Leu	Leu	Lys	Ile	Ser	Trp	Glu	Lys	
545					550					555					560	
CCA	GTC	TTT	CCA	GAG	AAT	AAC	CTT	CAA	TTC	CAG	ATT	CGC	TAT	GGT	TTA	1728
Pro	Val	Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	
				565				570						575		
AGT	GGA	AAA	GAA	GTA	CAA	TGG	AAG	ATG	TAT	GAG	GTT	TAT	GAT	GCA	AAA	1776
Ser	Gly	Lys	Glu	Val	Gln	Trp	Lys	Met	Tyr	Glu	Val	Tyr	Asp	Ala	Lys	
			580					585					590			
TCA	AAA	TCT	GTC	AGT	CTC	CCA	GTT	CCA	GAC	TTG	TGT	GCA	GTC	TAT	GCT	1824
Ser	Lys	Ser	Val	Ser	Leu	Pro	Val	Pro	Asp	Leu	Cys	Ala	Val	Tyr	Ala	
		595					600					605				
GTT	CAG	GTG	CGC	TGT	AAG	AGG	CTA	GAT	GGA	CTG	GGA	TAT	TGG	AGT	AAT	1872
Val	Gln	Val	Arg	Cys	Lys	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	
	610					615					620					
TGG	AGC	AAT	CCA	GCC	TAC	ACA	GTT	GTC	ATG	GAT	ATA	AAA	GTT	CCT	ATG	1920
Trp	Ser	Asn	Pro	Ala	Tyr	Thr	Val	Val	Met	Asp	Ile	Lys	Val	Pro	Met	
625					630					635					640	
AGA	GGA	CCT	GAA	TTT	TGG	AGA	ATA	ATT	AAT	GGA	GAT	ACT	ATG	AAA	AAG	1968
Arg	Gly	Pro	Glu	Phe	Trp	Arg	Ile	Ile	Asn	Gly	Asp	Thr	Met	Lys	Lys	

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645										650					655					
GAG	AAA	AAT	GTC	ACT	TTA	CTT	TGG	AAG	CCC	CTG	ATG	AAA	AAT	GAC	TCA	2016				
Glu	Lys	Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Met	Lys	Asn	Asp	Ser					
			660					665					670							
TTG	TGC	AGT	GTT	CAG	AGA	TAT	GTG	ATA	AAC	CAT	CAT	ACT	TCC	TGC	AAT	2064				
Leu	Cys	Ser	Val	Gln	Arg	Tyr	Val	Ile	Asn	His	His	Thr	Ser	Cys	Asn					
			675				680					685								
GGA	ACA	TGG	TCA	GAA	GAT	GTG	GGA	AAT	CAC	ACG	AAA	TTC	ACT	TTC	CTG	2112				
Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn	His	Thr	Lys	Phe	Thr	Phe	Leu					
			690			695					700									
TGG	ACA	GAG	CAA	GCA	CAT	ACT	GTT	ACG	GTT	CTG	GCC	ATC	AAT	TCA	ATT	2160				
Trp	Thr	Glu	Gln	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Ile	Asn	Ser	Ile					
705					710					715					720					
GGT	GCT	TCT	GTT	GCA	AAT	TTT	AAT	TTA	ACC	TTT	TCA	TGG	CCT	ATG	AGC	2208				
Gly	Ala	Ser	Val	Ala	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser					
				725					730					735						
AAA	GTA	AAT	ATC	GTG	CAG	TCA	CTC	AGT	GCT	TAT	CCT	TTA	AAC	AGC	AGT	2256				
Lys	Val	Asn	Ile	Val	Gln	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Asn	Ser	Ser					
			740					745					750							
TGT	GTG	ATT	GTT	TCC	TGG	ATA	CTA	TCA	CCC	AGT	GAT	TAC	AAG	CTA	ATG	2304				
Cys	Val	Ile	Val	Ser	Trp	Ile	Leu	Ser	Pro	Ser	Asp	Tyr	Lys	Leu	Met					
			755				760					765								
TAT	TTT	ATT	ATT	GAG	TGG	AAA	AAT	CTT	AAT	GAA	GAT	GGT	GAA	ATA	AAA	2352				
Tyr	Phe	Ile	Ile	Glu	Trp	Lys	Asn	Leu	Asn	Glu	Asp	Gly	Glu	Ile	Lys					
	770					775					780									
TGG	CTT	AGA	ATC	TCT	TCA	TCT	GTT	AAG	AAG	TAT	TAT	ATC	CAT	GGT	AAG	2400				
Trp	Leu	Arg	Ile	Ser	Ser	Ser	Val	Lys	Lys	Tyr	Tyr	Ile	His	Gly	Lys					
785					790					795					800					
TTT	ACT	ATA	CTT	TAG												2415				
Phe	Thr	Ile	Leu	*																
				805																

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 805 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ile	Cys	Gln	Lys	Phe	Cys	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Ile
1				5					10					15	
Tyr	Val	Ile	Thr	Ala	Phe	Asn	Leu	Ser	Tyr	Pro	Ile	Thr	Pro	Trp	Arg
			20					25					30		
Phe	Lys	Leu	Ser	Cys	Met	Pro	Pro	Asn	Ser	Thr	Tyr	Asp	Tyr	Phe	Leu
		35						40				45			

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Leu	Pro	Ala	Gly	Leu	Ser	Lys	Asn	Thr	Ser	Asn	Ser	Asn	Gly	His	Tyr
	50					55					60				
Glu	Thr	Ala	Val	Glu	Pro	Lys	Phe	Asn	Ser	Ser	Gly	Thr	His	Phe	Ser
65					70					75					80
Asn	Leu	Ser	Lys	Thr	Thr	Phe	His	Cys	Cys	Phe	Arg	Ser	Glu	Gln	Asp
				85					90					95	
Arg	Asn	Cys	Ser	Leu	Cys	Ala	Asp	Asn	Ile	Glu	Gly	Lys	Thr	Phe	Val
			100					105					110		
Ser	Thr	Val	Asn	Ser	Leu	Val	Phe	Gln	Gln	Ile	Asp	Ala	Asn	Trp	Asn
		115					120					125			
Ile	Gln	Cys	Trp	Leu	Lys	Gly	Asp	Leu	Lys	Leu	Phe	Ile	Cys	Tyr	Val
	130					135					140				
Glu	Ser	Leu	Phe	Lys	Asn	Leu	Phe	Arg	Asn	Tyr	Asn	Tyr	Lys	Val	His
145					150					155					160
Leu	Leu	Tyr	Val	Leu	Pro	Glu	Val	Leu	Glu	Asp	Ser	Pro	Leu	Val	Pro
				165					170					175	
Gln	Lys	Gly	Ser	Phe	Gln	Met	Val	His	Cys	Asn	Cys	Ser	Val	His	Glu
			180					185					190		
Cys	Cys	Glu	Cys	Leu	Val	Pro	Val	Pro	Thr	Ala	Lys	Leu	Asn	Asp	Thr
		195					200					205			
Leu	Leu	Met	Cys	Leu	Lys	Ile	Thr	Ser	Gly	Gly	Val	Ile	Phe	Gln	Ser
	210					215					220				
Pro	Leu	Met	Ser	Val	Gln	Pro	Ile	Asn	Met	Val	Lys	Pro	Asp	Pro	Pro
225					230					235					240
Leu	Gly	Leu	His	Met	Glu	Ile	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser
				245					250					255	
Trp	Ser	Ser	Pro	Pro	Leu	Val	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys
			260					265					270		
Tyr	Ser	Glu	Asn	Ser	Thr	Thr	Val	Ile	Arg	Glu	Ala	Asp	Lys	Ile	Val
		275					280					285			
Ser	Ala	Thr	Ser	Leu	Leu	Val	Asp	Ser	Ile	Leu	Pro	Gly	Ser	Ser	Tyr
	290					295					300				
Glu	Val	Gln	Val	Arg	Gly	Lys	Arg	Leu	Asp	Gly	Pro	Gly	Ile	Trp	Ser
305					310					315					320
Asp	Trp	Ser	Thr	Pro	Arg	Val	Phe	Thr	Thr	Gln	Asp	Val	Ile	Tyr	Phe
				325					330					335	
Pro	Pro	Lys	Ile	Leu	Thr	Ser	Val	Gly	Ser	Asn	Val	Ser	Phe	His	Cys
			340					345					350		
Ile	Tyr	Lys	Lys	Glu	Asn	Lys	Ile	Val	Pro	Ser	Lys	Glu	Ile	Val	Trp
		355					360					365			
Trp	Met	Asn	Leu	Ala	Glu	Lys	Ile	Pro	Gln	Ser	Gln	Tyr	Asp	Val	Val
	370					375					380				

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Ser	Asp	His	Val	Ser	Lys	Val	Thr	Phe	Phe	Asn	Leu	Asn	Glu	Thr	Lys
385					390					395					400
Pro	Arg	Gly	Lys	Phe	Thr	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	His
				405					410					415	
Glu	Cys	His	His	Arg	Tyr	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile
			420					425					430		
Asn	Ile	Ser	Cys	Glu	Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg
		435					440					445			
Trp	Ser	Thr	Ser	Thr	Ile	Gln	Ser	Leu	Ala	Glu	Ser	Thr	Leu	Gln	Leu
	450					455					460				
Arg	Tyr	His	Arg	Ser	Ser	Leu	Tyr	Cys	Ser	Asp	Ile	Pro	Ser	Ile	His
465					470					475					480
Pro	Ile	Ser	Glu	Pro	Lys	Asp	Cys	Tyr	Leu	Gln	Ser	Asp	Gly	Phe	Tyr
				485					490					495	
Glu	Cys	Ile	Phe	Gln	Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp
			500					505					510		
Ile	Arg	Ile	Asn	His	Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys
		515					520					525			
Val	Leu	Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Ser	Val	Lys
	530					535					540				
Ala	Glu	Ile	Thr	Ile	Asn	Ile	Gly	Leu	Leu	Lys	Ile	Ser	Trp	Glu	Lys
545					550					555					560
Pro	Val	Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu
				565					570					575	
Ser	Gly	Lys	Glu	Val	Gln	Trp	Lys	Met	Tyr	Glu	Val	Tyr	Asp	Ala	Lys
			580					585					590		
Ser	Lys	Ser	Val	Ser	Leu	Pro	Val	Pro	Asp	Leu	Cys	Ala	Val	Tyr	Ala
		595					600					605			
Val	Gln	Val	Arg	Cys	Lys	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn
	610					615					620				
Trp	Ser	Asn	Pro	Ala	Tyr	Thr	Val	Val	Met	Asp	Ile	Lys	Val	Pro	Met
625					630					635					640
Arg	Gly	Pro	Glu	Phe	Trp	Arg	Ile	Ile	Asn	Gly	Asp	Thr	Met	Lys	Lys
				645					650					655	
Glu	Lys	Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Met	Lys	Asn	Asp	Ser
			660					665					670		
Leu	Cys	Ser	Val	Gln	Arg	Tyr	Val	Ile	Asn	His	His	Thr	Ser	Cys	Asn
		675					680					685			
Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn	His	Thr	Lys	Phe	Thr	Phe	Leu
	690					695					700				
Trp	Thr	Glu	Gln	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Ile	Asn	Ser	Ile
705					710					715					720

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Gly	Ala	Ser	Val	Ala	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser
				725					730					735	
Lys	Val	Asn	Ile	Val	Gln	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Asn	Ser	Ser
			740					745					750		
Cys	Val	Ile	Val	Ser	Trp	Ile	Leu	Ser	Pro	Ser	Asp	Tyr	Lys	Leu	Met
		755					760					765			
Tyr	Phe	Ile	Ile	Glu	Trp	Lys	Asn	Leu	Asn	Glu	Asp	Gly	Glu	Ile	Lys
	770					775					780				
Trp	Leu	Arg	Ile	Ser	Ser	Ser	Val	Lys	Lys	Tyr	Tyr	Ile	His	Gly	Lys
785					790					795					800
Phe	Thr	Ile	Leu	*											
					805										

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGGATCCA TTATGTCTGC ACTCCGAAGG AAATTTG

37

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGAATTCT TATGTGAAGC GATCAGAGTT CATTTTTC

38

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGGGATCCG CTATGGCTGG TGATTCTAGG AATG

34

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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCGGAATTCC CCTCACACCG AGCCCCTGG

29

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAGGTGAGGG GCAAGAGACT GGATGG

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAAGCACATA CTGTTACGGT TCTGGCA

27

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAAGAATT GTTCCTGGGC ACAAGG

26

(2) INFORMATION FOR SEQ ID NO:18:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCATGAAAAG TACAGTACAC ATACCATGG

29

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTGAGCAGC AGCTGTGTCA TCCTT

25

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGTCATTCT GCTGCTTGTC GATAGC

26

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGTAAAGAC TGAAGTGGTA CTTCTC

26

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTAAAGTATA GTAACTTAC CATGG

25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATTATATG TATTAGGATG GTAGTATCC

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCTGTTAAGA AGTATTATAT CCATGGTAAG TTTACTATAC TTTAGTAATG AATGA

55

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGCTTCATTC ATTACTAAAG TATAGTAAAC TTACCATGGA TATAATACTT CTTAAC

56

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATCGTGCAGT CACTCAGTGC TTATCC

26

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGCCATCAAT TCAATTGGTG CTTCTGTTGC

30

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGAGCAATCC AGCCTACACA GTTGT CATG

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTGCAATGG AACATGGTCA GAAGATG

27

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